```
              GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:     November 6, 2004, 19:35:16 ; Search time 21.9375 Seconds
                                (without alignments)
                                39.474 Million cell updates/sec

Title:      US-10-618-644-4
Perfect score: 58
Sequence:   1 IPPGVPYWT 9

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:   283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:          283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_79;*
            1: pir1;*
            2: pir2;*
            3: pir3;*
            4: pir4;*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	58	100.0	212	2	JA0152	glycinin chain A7
2	58	100.0	560	2	S11004	glycinin G4 precur
3	58	100.0	562	2	S20946	glycinin Gy4 precu
4	58	100.0	563	2	S54802	glycinin A5A4B3 ch
5	57	98.3	136	2	T12140	legumin B - fava bea
6	57	98.3	564	2	S37241	legumin B - fava b
7	57	98.3	566	2	T06453	probable legumin B
8	52	89.7	562	1	FWSYG5	glycinin chain A5A
9	49	84.5	290	2	JC2097	legumin type B alp
10	49	84.5	484	2	A24942	legumin B4 precurs
11	49	84.5	485	2	S44268	legumin B precurso
12	49	84.5	500	2	S26688	legumin K - garden
13	49	84.5	503	2	S00336	legumin B LegJ pre
14	48	82.8	516	1	FWSYG3	glycinin G5 precur
15	43	74.1	168	2	T40893	hypothetical prote
16	42	72.4	503	2	E72078	probable sodium-tr
17	42	72.4	503	2	A86544	NADH (ubiquinone)
18	42	72.4	503	2	B81690	probable sodium-tr
19	42	72.4	503	2	C71535	probable NADH (ubi
20	42	72.4	705	2	S51635	fibroblast growth
21	42	72.4	707	2	A38429	keratinocyte growt
22	41	70.7	180	2	F72722	hypothetical prote
23	41	70.7	299	2	D95382	probable transcrip
24	41	70.7	379	2	T37274	probable cathepsin
25	41	70.7	2338	2	T25810	hypothetical prote
26	40	69.0	156	2	AG0243	probable exported
27	40	69.0	311	2	AB1880	hypothetical prote
28	40	69.0	353	2	AF0676	hydrogenase-1 oper
29	40	69.0	358	2	F64136	rnfD protein homol
30		39.5			T36209	probable pyridine
31		39			A22962	carbonate dehydrat
32		39			S07577	legumin storage pr
33		39			S07578	legumin storage pr
34		39			S07576	legumin storage pr
35		39			AF2460	glycosyltransferas
36		39			S51767	glycosyl transfera
37		39			A55197	Wiskott-Aldrich sy
38		39			H83362	gluconate dehydrog
39		39			D90483	alpha-xylosidase (
40		39			T35389	probable serine-th
41		39			D82436	transporter, AcrB/
42		39			T01916	hypothetical prote
43		39			T08196	hypothetical prote
44		39			T18968	probable serine-ty
45		39			T30939	hemocyanin G-type

Note: the Score column values for rows 30–45 read 39.5, 39, 39, … and the Match columns show 68.1, 67.2, 67.2 … (454, 235, 329, 335, 335, 382, 433, 502, 591, 731, 783, 1067, 1095, 1174, 2105, 2896) with DB 2.

ALIGNMENTS

```
RESULT 1
JA0152
glycinin chain A7 - soybean
N;Alternate names: seed storage protein
C;Species: Glycine max (soybean)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 24-Feb-1995
C;Accession: JA0152
R;Kagawa, H.; Hirano, H.
Plant Sci. 56, 189-195, 1988
A;Title: Identification and structural characterization of the glycinin seed storage pr
A;Reference number: JA0152
A;Accession: JA0152
A;Molecule type: protein
A;Residues: 1-212 <KAG>
A;Experimental source: seed
C;Comment: Glycinin is the most abundant protein in the soybean seeds. A7 chain is one ...
C;Superfamily: glycinin

Query Match          100.0%;  Score 58; DB 2;  Length 212;
Best Local Similarity 100.0%;  Pred. No. 0.047;
Matches   9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy     1 IPPGVPYWT 9
           |||||||||
Db    29 IPPGVPYWT 37

RESULT 2
S11004
glycinin G4 precursor - soybean
C;Species: Glycine max (soybean)
C;Date: 21-Nov-1993 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: S11004
R;Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thanh, V.H.; Scallon, B.J.; Fischer, R.L.;
Plant Cell 1, 313-328, 1989
A;Title: Characterization of the glycinin gene family in soybean.
A;Reference number: S10851; MUID:92393391; PMID:2485233
A;Accession: S11004
A;Molecule type: DNA
A;Residues: 1-560 <NIE>
A;Cross-references: UNIPROT:Q9S9D0
A;Experimental source: variety Dare
C;Genetics:
A;Gene: Gy4
C;Superfamily: glycinin
C;Keywords: storage protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-560/Product: glycinin G4 #status predicted <MAT>

Query Match          100.0%;  Score 58; DB 2;  Length 560;
Best Local Similarity 100.0%;  Pred. No. 0.13;
Matches   9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

```
Qy    1 IPPGVPYWT 9
        |||||||||
Db  149 IPPGVPYWT 157
```

RESULT 3
S20946
glycinin Gy4 precursor - soybean (cv. Forrest)
C;Species: Glycine max (soybean)
A;Variety: cv. Forrest
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S20946
R;Xue, Z.T.; Xu, M.L.; Shen, W.; Zhuang, N.L.; Hu, W.M.; Shen, S.C.
Plant Mol. Biol. 18, 897-908, 1992
A;Title: Characterization of a Gy4 glycinin gene from soybean Glycine max cv. Forrest.
A;Reference number: S20946; MUID:92256811; PMID:1316192
A;Accession: S20946
A;Molecule type: DNA
A;Residues: 1-562 <XUE>
A;Cross-references: UNIPROT:Q43452; EMBL:X52863; NID:g18640; PIDN:CAA37044.1; PID:g18641
C;Genetics:
A;Gene: Gy4
A;Introns: 97/1; 184/3; 433/3
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-562/Product: glycinin Gy4 #status predicted <MAT>

```
Query Match       100.0%;  Score 58;  DB 2;  Length 562;
Best Local Similarity  100.0%;  Pred. No. 0.13;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 IPPGVPYWT 9
        |||||||||
Db  148 IPPGVPYWT 156
```

RESULT 4
S54802
glycinin A5A4B3 chain - soybean
C;Species: Glycine max (soybean)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S54802
R;Xue, Z.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54802
A;Accession: S54802
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-563 <XUE>
A;Cross-references: UNIPROT:Q39921; EMBL:X86970; NID:g806555; PIDN:CAA60533.1; PID:g8065
C;Superfamily: glycinin

```
Query Match       100.0%;  Score 58;  DB 2;  Length 563;
Best Local Similarity  100.0%;  Pred. No. 0.13;
Matches  9;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 IPPGVPYWT 9
        |||||||||
Db  149 IPPGVPYWT 157
```

RESULT 5
T12140
legumin - fava bean (fragment)
C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12140
R;Heim, U.; Baeumlein, H.; Wobus, U.
Plant Mol. Biol. 25, 131-135, 1994
A;Title: The legumin gene family: a reconstructed Vicia faba legumin gene encoding a hig

A;Reference number: S46503; MUID:94272010; PMID:8003694
A;Accession: T12140
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <HEI>
A;Cross-references: UNIPROT:Q43672; EMBL:Z26487; NID:g403333; PIDN:CAA81261.1; PID:g4033
C;Genetics:
A;Gene: LeiB161
A;Note: intron positions not resolved (incomplete sequence)
C;Superfamily: glycinin
C;Keywords: seed; storage protein

```
Query Match       98.3%;  Score 57;  DB 2;  Length 136;
Best Local Similarity  88.9%;  Pred. No. 0.042;
Matches  8;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 IPPGVPYWT 9
        ||||:||||
Db   50 IPPGIPYWT 58
```

RESULT 6
S37241
legumin B - fava bean (fava bean)
C;Species: Vicia faba (fava bean)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S46503; S37241
R;Heim, U.; Baeumlein, H.; Wobus, U.
Plant Mol. Biol. 25, 131-135, 1994
A;Title: The legumin gene family: a reconstructed Vicia faba legumin gene encoding a hig
A;Reference number: S46503; MUID:94272010; PMID:8003694
A;Accession: S46503
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-564 <HE2>
A;Cross-references: UNIPROT:Q43673; EMBL:Z26489; NID:g403335; PIDN:CAA81262.1; PID:g4033
C;Genetics:
A;Introns: 178/3; 439/3
C;Superfamily: glycinin

```
Query Match       98.3%;  Score 57;  DB 2;  Length 564;
Best Local Similarity  88.9%;  Pred. No. 0.19;
Matches  8;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 IPPGVPYWT 9
        ||||:||||
Db  142 IPPGIPYWT 150
```

RESULT 7
T06453
probable legumin B - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06453
R;Bown, D.P.
submitted to the EMBL Data Library, June 1992
A;Reference number: Z15688
A;Accession: T06453
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-566 <BOW>
A;Cross-references: UNIPROT:O24294; EMBL:X67424; PIDN:CAA47809.1
A;Experimental source: cv. Feltham First
C;Genetics:
A;Gene: legS
C;Superfamily: glycinin
C;Keywords: seed; storage protein

```
Query Match       98.3%;  Score 57;  DB 2;  Length 566;
Best Local Similarity  88.9%;  Pred. No. 0.19;
Matches  8;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;
```

RESULT 8
FWSYG5
glycinin chain A5A4B3 precursor - soybean
N;Alternate names: 11S globulin
C;Species: Glycine max (soybean)
C;Date: 28-Feb-1986 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A91145; A91133; A03348; A25207; A27253
R;Momma, T.; Negoro, T.; Hirano, H.; Matsumoto, A.; Udaka, K.; Fukazawa, C.
Eur. J. Biochem. 149, 491-496, 1985
A;Title: Glycinin A5A4B3 mRNA: cDNA cloning and nucleotide sequencing of a splitting sto
A;Reference number: A91145; MUID:85230642; PMID:2988947
A;Accession: A91145
A;Molecule type: mRNA
A;Residues: 1-562 <MOM>
A;Cross-references: UNIPROT:P02858; GB:X02626; NID:g18628; PIDN:CAA26478.1; PID:g732706
A;Experimental source: cv. Bonminori
A;Note: the authors translated the codon TCA for residue 86 as Leu, GAC for residue 145
R;Hirano, H.; Fukazawa, C.; Harada, K.
FEBS Lett. 181, 124-128, 1985
A;Title: The primary structures of the A4 and A5 subunits are highly homologous to that
A;Reference number: A91333
A;Accession: A91333
A;Molecule type: protein
A;Residues: 24-28,'F',30-81,'L',83-85,'L',87-93,'V',95-100,'I',102,'M',104,'F',106-116,'
A;Experimental source: cv. Bonminori
A;Note: parts of the A4 chain, including the amino end, were sequenced
C;Comment: The source of this protein was cotyledon tissue taken from seeds at the middl
C;Comment: The glycinin molecule, the major seed storage protein of soybean, is composed
identified.
C;Comment: Acidic (A5 and A4) and basic (B3) components of this glycinin subunit are syn
sulfide bond, that is thought to be noncovalently associated with the A4 chain.
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-120/Product: glycinin, A5 chain #status experimental <GA5>
F;121-377/Product: glycinin, A4 chain #status predicted <GA4>
F;378-562/Product: glycinin, B3 chain #status predicted <GB3>
F;108-384/Disulfide bonds: #status predicted

Query Match   89.7%; Score 52; DB 1; Length 562;
Best Local Similarity   88.9%; Pred. No. 1.1;
Matches   8; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 IPPGVPYWT 9
          ||| |||||
Db   149 IPPSVPYWT 157

RESULT 9
JC2097
legumin type B alpha chain precursor (clone LeB4, B4) - tick bean
C;Species: Vicia faba var. minor (tick bean)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 06-Dec-1996
C;Accession: JC2097
R;Horstmann, C.; Schlesier, B.; Otto, A.; Kostka, S.; Muentz, K.
Theor. Appl. Genet. 86, 867-874, 1993
A;Title: Polymorphism of legumin subunits from field bean (Vicia faba L. var. minor) and
A;Reference number: JC2094
A;Accession: JC2097
A;Molecule type: DNA
A;Residues: 1-290 <HOR>
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-268/Product: legumin type B alpha chain #status predicted <MAT>

Query Match   84.5%; Score 49; DB 2; Length 290;
Best Local Similarity   77.8%; Pred. No. 1.7;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 IPPGVPYWT 9
          ||| :||||
Db   147 IPSGIPYWT 155

RESULT 10
A24942
legumin B4 precursor - fava bean
C;Species: Vicia faba (fava bean)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 13-Nov-1998
C;Accession: A24942
R;Baeumlein, H.; Wobus, U.; Pustell, J.; Kafatos, F.C.
Nucleic Acids Res. 14, 2707-2720, 1986
A;Title: The legumin gene family: structure of a B type gene of Vicia faba and a possib
A;Reference number: A24942; MUID:86176760; PMID:3960730
A;Accession: A24942
A;Molecule type: DNA
A;Residues: 1-484 <BAE>
A;Note: the authors translated the codon GTT for residue 188 as Gly and CAC for residue
C;Superfamily: glycinin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-483/Product: legumin B4 #status predicted <MAT>

Query Match   84.5%; Score 49; DB 2; Length 484;
Best Local Similarity   77.8%; Pred. No. 2.9;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 IPPGVPYWT 9
          ||| :||||
Db   147 IPSGIPYWT 155

RESULT 11
S44268
legumin B precursor - spring vetch
C;Species: Vicia sativa (spring vetch, tare)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: S44268
R;Nong, V.; Becker, C.; Muentz, K.
submitted to the EMBL Data Library, April 1994
A;Description: Cloning and heterologous expression of cDNAs encoding legumins of vetch
A;Reference number: S44266
A;Accession: S44268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-485 <NON>
A;Cross-references: UNIPROT:Q41703; EMBL:Z32796; NID:g479103; PIDN:CAA83674.1; PID:g479
C;Superfamily: glycinin

Query Match   84.5%; Score 49; DB 2; Length 485;
Best Local Similarity   77.8%; Pred. No. 2.9;
Matches   7; Conservative   1; Mismatches   1; Indels   0; Gaps   0;

Qy   1 IPPGVPYWT 9
          ||| :||||
Db   152 IPSGIPYWT 160

RESULT 12
S26688
legumin K - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 12-Apr-1995
C;Accession: S26688
R;Thompson, A.J.; Bown, D.; Yaish, S.; Gatehouse, J.A.
Biochem. Physiol. Pflanz. 187, 1-12, 1991
A;Title: Differential expression of seed storage protein genes in the pea legJ subfamil
A;Reference number: S26688
A;Accession: S26688
A;Status: preliminary
A;Molecule type: DNA

```
A;Title: Characterization of the glycinin gene family in soybean.
A;Reference number: S10851; MUID:92393391; PMID:2485233
A;Accession: S11005
A;Molecule type: DNA
A;Residues: 1-516 <NIE>
A;Experimental source: variety Forrest
C;Genetics:
A;Gene: Gy5
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-344/Product: glycinin chain A3 #status predicted <GLA>
F;345-516/Product: glycinin chain B4 #status predicted <GLB>
F;109-351/Disulfide bonds: #status predicted

Query Match             82.8%;  Score 48; DB 1;  Length 516;
Best Local Similarity   88.9%;  Pred. No. 4.5;
Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 IPPGVPYWT 9
            || ||||||
Db    149 IPLGVPYWT 157

RESULT 15
T40893
hypothetical protein SPCC1259.04 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40893
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z21955
A;Accession: T40893
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-168 <WOO>
A;Cross-references: UNIPROT:O94704; EMBL:AL034564; PIDN:CAA22542.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h- strain 972h; cosmid c1259
C;Genetics:
A;Gene: SPDB:SPCC1259.04
A;Map position: 3
A;Introns: 47/2

Query Match             74.1%;  Score 43; DB 2;  Length 168;
Best Local Similarity   85.7%;  Pred. No. 8.7;
Matches    6;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    0;

Qy      2 PPGVPYW 8
            ||| ||
Db     68 PPGSPYW 74

Search completed: November  6, 2004, 19:54:15
Job time : 23.9375 secs
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```
A;Residues: 1-500 <THO>
A;Cross-references: EMBL:X67423
C;Genetics:
A;Start codon: GTG
A;Introns: 183/3; 375/3
C;Superfamily: glycinin

Query Match             84.5%;  Score 49; DB 2;  Length 500;
Best Local Similarity   77.8%;  Pred. No. 3;
Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 IPPGVPYWT 9
            || |:|:|||
Db    147 IPSGIPYWT 155

RESULT 13
S00336
legumin B LegJ precursor - garden pea
N;Alternate names: minor legumin LegJ
C;Species: Pisum sativum (garden pea)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S00336
R;Gatehouse, J.A.; Bown, D.; Gilroy, J.; Levasseur, M.; Castleton, J.; Ellis, T.H.N.
Biochem. J. 250, 15-24, 1988
A;Title: Two genes encoding 'minor' legumin polypeptides in pea (Pisum sativum L.). Char
A;Reference number: S00336; MUID:88183306; PMID:3355508
A;Accession: S00336
A;Molecule type: DNA
A;Residues: 1-503 <GAT>
A;Cross-references: UNIPROT:P05692; EMBL:X07014; NID:g20782; PIDN:CAA30067.1; PID:g20783
A;Note: part of this sequence, including the amino end of both the alpha and beta chains
C;Genetics:
A;Gene: LegJ
A;Introns: 183/3; 378/3
C;Superfamily: glycinin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-322/Product: legumin B alpha chain #status experimental <ACH>
F;323-503/Product: legumin B beta chain #status experimental <BCH>

Query Match             84.5%;  Score 49; DB 2;  Length 503;
Best Local Similarity   77.8%;  Pred. No. 3.1;
Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 IPPGVPYWT 9
            || |:|:|||
Db    147 IPSGIPYWT 155

RESULT 14
FWSYG3
glycinin G5 precursor - soybean
N;Alternate names: 11S globulin; glycinin A3B4
C;Species: Glycine max (soybean)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A92524; S11005; A05083; A22615
R;Fukazawa, C.; Momma, T.; Hirano, H.; Harada, K.; Udaka, K.
J. Biol. Chem. 260, 6234-6239, 1985
A;Title: Glycinin A3B4 mRNA: cloning and sequencing of double-stranded cDNA complementar
A;Reference number: A92524; MUID:85207609; PMID:3838983
A;Accession: A92524
A;Molecule type: mRNA
A;Residues: 1-516 <FUK>
A;Cross-references: UNIPROT:P04347; GB:M10962; NID:g169968; PIDN:AAA33964.1; PID:g169969
A;Experimental source: cv. Bonminori
R;Hirano, H.; Fukazawa, C.; Harada, K.
J. Biol. Chem. 259, 14371-14377, 1984
A;Title: The complete amino acid sequence of the A-3 subunit of the glycinin seed storag
A;Reference number: A92465; MUID:85054904; PMID:6542104
A;Contents: annotation
A;Note: the sequence reported is very different from that shown
R;Nielsen, N.C.; Dickinson, C.D.; Cho, T.J.; Thanh, V.H.; Scallon, B.J.; Fischer, R.L.;
Plant Cell 1, 313-328, 1989
```